

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Rezaie, Alireza
Esmon, Charles
- (ii) TITLE OF INVENTION: Calcium Binding Recombinant Antibody
Against Protein C
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Patrea L. Pabst
 - (B) STREET: 1100 Peachtree Street, Suite 2800
 - (C) CITY: Atlanta
 - (D) STATE: Georgia
 - (E) COUNTRY: USA
 - (F) ZIP: 30309-4530
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: Jun 9, 1994
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/982,832
 - (B) FILING DATE: 30-NOV-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/730,040 (U.S. Patent No. 5,202,253)
 - (B) FILING DATE: 12-JUL-1991
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/292,447
 - (B) FILING DATE: 30-DEC-1988
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Pabst, Patrea L.
 - (B) REGISTRATION NUMBER: 31,284
 - (C) REFERENCE/DOCKET NUMBER: OMRF106CIP

(ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: (404) 815-6508
 (B) TELEFAX: (404) 815-6555

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: Internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGCGGCCGC TGGATAGACA GATGGGGGTG TCGTTTTGCC

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGCGGCCGC CCCCCCCCCC CCCCCCCCCC

- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: YES
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAGCGGCCGC GAAGATGGAT ACAGTTGGTG CAGCATCAGC

- (2) INFORMATION FOR SEQ ID NO:5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGTTACTCT GCTCGAGTCT GGCCCTGG

- (2) INFORMATION FOR SEQ ID NO:6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGGCCTACTA GTTTACTAAC AATCCCTGGG CACAAT

- (2) INFORMATION FOR SEQ ID NO:7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGTCCAGAGG AGAGCTCATT CTCACCCAGT CTCCGGC

- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: YES
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCCTTCTAGA TTACTAACAC TCTCCCCTGT TGAA

- (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION: 1..57
 - (D) OTHER INFORMATION: /note= "Signal peptide encoded by nucleotides 1 through 57."
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION: 58..417
 - (D) OTHER INFORMATION: /note= "Mature peptide encoded by nucleotides 58 through 417."
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGGCAGGC TTTCTTCTTC ATTCTTGCTA CTGATTGCCC CTGCATATGT CCTGTCCCAG	60
GTTACTCTGA AAGAGTCTGG CCCTGGGATA TTGCAGCCCT CCCAGACCCT CACTCTGACT	120
TGTTCTCTCT CTGGGTTTTTC ACTGAGGACT TCTGGTATGG GTGTAGGCTG GATTCGTCAG	180
CCTTCAGGGA AGGGTCTGGA GTGGCTGGCA CACATTTGGT GGGATGATGA CAAGCGCTAT	240
AACCCAGTCC TGAAGAGCCG ACTGATAATC TCCAAGGATA CCTCCAGGAA ACAGGTATTC	300
CTCAAGATCG CCAGTGTGGA CACTGCAGAT ACTGCCACAT ACTACTGTGT TCGAATGATG	360
GATGATTACG ACGCTATGGA CTA CTGGGGT CAAGGAACCT CAGTCACCGT CTCCTCT	417

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: Internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 20..139
 - (D) OTHER INFORMATION: /note= "Gln at position 20 starts mature peptide."
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gly Arg Leu Ser Ser Ser Phe Leu Leu Leu Ile Ala Pro Ala Tyr
 1 5 10 15

Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
 20 25 30

Pro Ser Gln Thr Leu Thr Leu Thr Cys Ser Leu Ser Gly Phe Ser Leu
 35 40 45

Arg Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys
 50 55 60

Gly Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
 65 70 75 80

Asn Pro Val Leu Lys Ser Arg Leu Ile Ile Ser Lys Asp Thr Ser Arg
 85 90 95

Lys Gln Val Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala
 100 105 110
 Thr Tyr Tyr Cys Val Arg Met Met Asp Asp Tyr Asp Ala Met Asp Tyr
 115 120 125
 Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 130 135

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HPC-4 Light Chain Variable Region (VL Kappa)

(ix) FEATURE:

- (A) NAME/KEY: misc feature

- (B) LOCATION: 1..66

(D) OTHER INFORMATION: /note= "Signal peptide encoded by nucleotides 1 through 66."

(ix) FEATURE:

- (A) NAME/KEY: misc feature

- (B) LOCATION: 67..387

(D) OTHER INFORMATION: /note= "Mature peptide encoded by nucleotides 67 through 387."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGATTTTC AGGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCCTCAGT CATAATGTCC	60
AGAGGACAAA TTATTCTCAC CCAGTCTCCG GCAATCATGT CTGCATCTCT GGGGGAGGAG	120
ATCACCTTAA CCTGCAGTGC CACTTCGAGT GTAACCTACG TCCACTGGTA CCAGCAGAAG	180

TCAGGCACTT CTCCCAAACCT CTTGATTTAT GGGACATCCA ACCTGGCTTC TGGAGTCCCT 240
TCTCGTTTCA GTGGCAGTGG GTCTGGGACC TTTTATTCTC TCACAGTCAG CAGTGTGGAG 300
GCTGAAGATG CTGCCGATTA TTA CTGCCAT CAGTGGAATA GTTATCCGCA CACGTTCGGA 360
GGGGGGACCA AGCTGGAAAT AAAACGG 387

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HPC-4 Light Chain Variable Region (VL Kappa)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 23...129

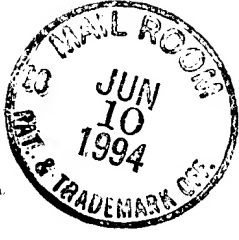
(D) OTHER INFORMATION: /note= "Gln at position 23 starts mature peptide."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5				10					15		
Val	Ile	Met	Ser	Arg	Gly	Gln	Ile	Ile	Leu	Thr	Gln	Ser	Pro	Ala	Ile
			20				25					30			
Met	Ser	Ala	Ser	Leu	Gly	Glu	Glu	Ile	Thr	Leu	Thr	Cys	Ser	Ala	Thr
		35				40						45			

Ser	Ser	Val	Thr	Tyr	Val	His	Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Thr	Ser
50						55					60				
Pro	Lys	Leu	Leu	Ile	Tyr	Gly	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65					70					75					80
Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Phe	Tyr	Ser	Leu	Thr	Val
				85					90					95	
Ser	Ser	Val	Glu	Ala	Glu	Asp	Ala	Ala	Asp	Tyr	Tyr	Cys	His	Gln	Trp
			100					105					110		
Asn	Ser	Tyr	Pro	His	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys
		115					120					125			

Arg



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Rezaie, Alireza
Esmon, Charles

(ii) TITLE OF INVENTION: Calcium Binding Recombinant Antibody
Against Protein C

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Patrea L. Pabst
(B) STREET: 1100 Peachtree Street, Suite 2800
(C) CITY: Atlanta
(D) STATE: Georgia
(E) COUNTRY: USA
(F) ZIP: 30309-4530

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/982,832
(B) FILING DATE: 30-NOV-1992

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/730,040 (U.S. Patent No. 5,202,253)

2

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGCGGCCGC TGGATAGACA GATGGGGGTG TCGTTTGGCC

40

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGCGGCCGC CCCCCCCCCC CCCCCCCCCC

30

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAGCGGCCGC GAAGATGGAT ACAGTTGGTG CAGCATCAGC

(2) INFORMATION FOR SEQ ID NO:5:

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGTACTCT GCTCGAGTCT GGCCCTGG

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

28

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGGCCTACTA GTTACTAAC AATCCCTGGG CACAAT

36

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGTCCAGAGG AGAGCTCATT CTCACCCAGT CTCGGG

37

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCCTTCTAGA TTACTAACAC TCTCCCTGT TGAA

34

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 417 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..57

(D) OTHER INFORMATION: /note= "Signal peptide encoded by nucleotides 1 through

57."

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 58..417
- (D) OTHER INFORMATION: /note= "Mature peptide encoded by nucleotides 58 through 417."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGGCAGGC TTTCTTCTTC ATTCTTGCTA CTGATTGCCC CTGCATATGT CCTGTCCCAG	60
GTTACTCTGA AAGAGTCTGG CCCTGGGATA TTGCAGCCCT CCCAGACCCT CACTCTGACT	120
TGTTCTCTCT CTGGGTTTTC ACTGAGGACT TCTGGTATGG GTGTAGGCTG GATTCTGTCAG	180
CCTTCAGGGA AGGCTCTGGA GTGGCTGGCA CACATTTGGT GGGATGATGA CAAAGCGCTAT	240
AACCCAGTCC TGAAGAGCCG ACTGATAATC TCCAAGGATA CCTCCAGGAA ACAGGTATTC	300
CTCAAGATCG CCAGTGTGGA CACTGCAGAT ACTGCCACAT ACTACTGTGT TCGAATGATG	360
GATGATTACG ACGCTATGGA CTACTGGGGT CAAGGAACCT CAGTCACCGT CTCCTCT	417

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: Internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 20..139

(D) OTHER INFORMATION: /note= "Gln at position 20 starts mature peptide."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gly Arg Leu Ser Ser Ser Phe Leu Leu Leu Ile Ala Pro Ala Tyr
1 5 10 15

Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
20 25 30

Pro Ser Gln Thr Leu Thr Leu Thr Cys Ser Leu Ser Gly Phe Ser Leu
35 40 45

Arg Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys
50 55 60

Gly Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Lys Arg Tyr
65 70 75 80

Asn Pro Val Leu Lys Ser Arg Leu Ile Ile Ser Lys Asp Thr Ser Arg
85 90 95

Lys Gln Val Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala
100 105 110

Thr Tyr Tyr Cys Val Arg Met Met Asp Asp Tyr Asp Ala Met Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
130 135

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HPC-4 Light Chain Variable Region (VL Kappa)

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: /note= "Signal peptide encoded by nucleotides 1 through 66."

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 67..387
- (D) OTHER INFORMATION: /note= "Mature peptide encoded by nucleotides 67 through 387."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGATTTC	AGGTGCAGAT	TTTCAGCTTC	CTGCTAATCA	GTGCCTCAGT	CATAATGTCC	60
AGAGGACAAA	TTATTCTCAC	CCAGTCTCCG	GCAATCATGT	CTGCATCTCT	GGGGGAGGAG	120
ATCACCCCTAA	CCTGCAGTGC	CAC TTCGAGT	GTAAC TTACG	TCCACTGGTA	CCAGCAGAAG	180

TCAGGCACTT CTCCCAAACT CTTGATTTAT GGGACATCCA ACCTGGCTTC TGGAGTCCCT	240
TCCTCGTTTCA GTGGCAGTGG GTCTGGGACC TTTTATTCTC TCACAGTCAG CAGTGTGGAG	300
GCTGAAGATG CTGCCGATTA TTA CTGCCAT CAGTGGAATA GTTATCCGCA CACGTTCCGA	360
GGGGGGACCA AGCTGGAAAT AAAACGG	387

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HPC-4 Light Chain Variable Region (VL Kappa)

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 23..129
- (D) OTHER INFORMATION: /note= "Gln at position 23 starts mature peptide."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	

Val Ile Met Ser Arg Gly Gln Ile Ile Leu Thr Gln Ser Pro Ala Ile
 20 25 30
 Met Ser Ala Ser Leu Gly Glu Ile Thr Leu Thr Cys Ser Ala Thr
 35 40 45
 Ser Ser Val Thr Tyr Val His Trp Tyr Gln Gln Lys Ser Gly Thr Ser
 50 55 60
 Pro Lys Leu Leu Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Phe Tyr Ser Ser Leu Thr Val
 85 90 95
 Ser Ser Val Glu Ala Glu Asp Ala Ala Asp Tyr Tyr Cys His Gln Trp
 100 105 110
 Asn Ser Tyr Pro His Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 115 120 125

Arg